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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file seq1-3_5.res made by mruhl on Wed 22 Jan 103 17:05:36-PST.

Query sequence being compared: US-09-894-657-1 (1-168)
Number of sequences searched: 6
Number of scores above cutoff: 6

Results of the initial comparison of US-09-894-657-1 (1-168) with:
File : US09894657.pep

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100-
N -
U -
M -
B -
R -
O -
F -
S -
E -
U -
E -
N -
C -
S -
SCORE 0 191 37 56 75 93 112 131 149 168
STDDEV 0 1 1 1 1 1 1 1 1 1

```

PARAMETERS

Similarity matrix PAM-150 K-tuple 2
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 168
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 60 Median 13 Standard Deviation 78.39
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 2027
Number of sequences searched: 6
Number of scores above cutoff: 6

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Score	Signif. Frame

1. US-09-894-657-1 Sequence 1, Application US 168 168 168 1.38 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Score	Signif. Frame
2. US-09-894-657-7 Sequence 7, Application US	168 154 154 1.20 0				
3. US-09-894-657-9 Sequence 9, Application US	469 12 81 -0.61 0				
4. US-09-894-657-5 Sequence 5, Application US	469 12 81 -0.61 0				
5. US-09-894-657-8 Sequence 8, Application US	313 7 76 -0.68 0				
6. US-09-894-657-3 Sequence 3, Application US	440 7 76 -0.68 0				

1. US-09-894-657-1 (1-168)
US-09-894-657-1 Sequence 1, Application US/09894657

Initial Score	168	Optimized score	168	Significance	1.38
Residue Identity	100%	Matches	168	Mismatches	0
Gaps	0	Conservative Substitutions			0

```

X 10 20 30 40 50 60 70
MFOIPEPEPSEQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLMDASHQOEOPTSSHHGACAVEIRSR
MFOIPEPEPSEQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLMDASHQOEOPTSSHHGACAVEIRSR
X 10 20 30 40 50 60 70

```

```

80 90 100 110 120 130 140
HSSYPAGTEDEDEGGEPPSPRGRSRSPNLMMAQRYGRELRRMSDFVDSFKKGLPRPKSAGTATQWRQS
HSSYPAGTEDEGGEPPSPRGRSRSPNLMMAQRYGRELRRMSDFVDSFKKGLPRPKSAGTATQWRQS
HSSYPAGTEDEGGEPPSPRGRSRSPNLMMAQRYGRELRRMSDFVDSFKKGLPRPKSAGTATQWRQS
80 90 100 110 120 130 140

```

```

150 160
SSWTFRVFOQSMWMDRNLGRGSSAPSO
SSWTFRVFOQSMWMDRNLGRGSSAPSO
SSWTFRVFOQSMWMDRNLGRGSSAPSO
150 160

```

2. US-09-894-657-1 (1-168)
US-09-894-657-7 Sequence 7, Application US/09894657

Initial Score	154	Optimized score	154	Significance	1.20
Residue Identity	85%	Matches	143	Mismatches	24
Gaps	0	Conservative Substitutions			1

```

X 10 20 30 40 50 60 70
MFOIPEPEPSEQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLMDASHQOEOPTSSHHGACAVEIRSR
MFOIPEPEPSEQEDSSAERGLGSPAGDGPSSGSKHHRQAPGLMDASHQOEOPTSSHHGACAVEIRSR
X 10 20 30 40 50 60 70

```

```

80 90 100 110 120 130 140
HSSYPAGTEDEDEGGEPPSPRGRSRSPNLMMAQRYGRELRRMSDFVDSFKKGLPRPKSAGTATQWRQS
HSSYPAGTEDEDEGGEPPSPRGRSRSPNLMMAQRYGRELRRMSDFVDSFKKGLPRPKSAGTATQWRQS
HSSYPAGTEDEDEGGEPPSPRGRSRSPNLMMAQRYGRELRRMSDFVDSFKKGLPRPKSAGTATQWRQS
80 90 100 110 120 130 140

```

```

150 160
SSWTFRVFOQSMWMDRNLGRGSSAPSO
SSWTFRVFOQSMWMDRNLGRGSSAPSO
SSWTFRVFOQSMWMDRNLGRGSSAPSO
150 160

```

3. US-09-894-657-1 (1-168)
US-09-894-657-9 Sequence 9, Application US/09894657

Initial Score	12	Optimized score	81	Significance	-0.61

EQLDPKPQVSGRPVIKPEVDSTFCHNV
220 230 240

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FastDB - Fast Pairwise Comparison of Sequences

Release 5.4

Results file seq3-5.res made by mrnh1 on Wed 22 Jan 103 17:09:59-PST.

Query sequence being compared:	US-09-894-657-3 (1-440)
Number of sequences searched:	6
Number of scores above cutoff:	6

Results of the initial comparison of US-09-894-657-3 (1-440) with
File : US09894657.pep

[illegible]

PARAMETERS		
Similarity matrix	PAM-150	2
Threshold level of sim.	16%	
Mismatch penalty	1	200
Gap penalty	5.00	Window size
Gap size penalty	0.05	
Cutoff score	1	
Randomization group	0	

SEARCH STATISTICS		
Scores:	Mean 116	Median 9
Times:	CPU 00:00:00.00	Total elapsed 00:00:00.00
Number of residues:		2027
Number of sequences searched:		6
Number of scores above cutoff:		6

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Init. Opt.	Length	Score	Score	Sig.	Frame
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1. US-09-894-657-3 Sequence 3, Application US	440	440	440	1.78	0
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Sequence Name	Description	Length	Int. Score	Opt. Score	Sig. Frame
2. US-09-894-657-8	Sequence 8, Application US	313	229	305	0.62 0
3. US-09-894-657-9	Sequence 9, Application US	469	8	184	-0.59 0
4. US-09-894-657-5	Sequence 5, Application US	469	8	185	-0.59 0

1. US-09-894-657-3 (1-440)
US-09-894-657-3 Sequence 3, Application US/09894657

```
Initial Score = 440 Optimized Score = 440 Significance = 1.78
Residue Identity = 100% Matches = 440 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0
```

X 10 20 30 40 50 60 70
 MRVYIVILLCFCAAEALRRKSPGVSRYVNHGAGGGRGSPVRYRYAPGLPCDDVYTYLHKHYLDCORR
 MRVYIVILLCFCAAEALRRKSPGVSRYVNHGAGGGRGSPVRYRYAPGLPCDDVYTYLHKHYLDCORR
 X 10 20 30 40 50 60 70

	80	90	100	110	120	130	140
YYVLPGWQDILLHMLRNKIRLKNMFSFKKLSLDLOONEISEAFFGNGKLTTLLLOHNQIKVLN							
YYVLPGWQDILLHMLRNKIRLKNMFSFKKLSLDLOONEISEAFFGNGKLTTLLLOHNQIKVLN							
YYVLPGWQDILLHMLRNKIRLKNMFSFKKLSLDLOONEISEAFFGNGKLTTLLLOHNQIKVLN							
	80	90	100	110	120	130	140

TEEVYIYPLLSYLRKLVNDHPHCHCEETLISMOJPRNNLGNVAKCSPOEOKKKRLROIKSOLCNEEFK
150 160 170 180 190 200 210

TEEVYIYPLLSYLRKLVNDHPHCHCEETLISMOJPRNNLGNVAKCSPOEOKKKRLROIKSOLCNEEFK
150 160 170 180 190 200 210

220 230 240 250 260 270 280
 EOLDPKPOVSGSRPVIKPEVDSFGCHNYVPIOTLCKRKELKKVNNNIPDVLKDLSTYKNIINDLRPEEFEEF
 EOLDPKPOVSGSRPVIKPEVDSFGCHNYVPIOTLCKRKELKKVNNNIPDVLKDLSTYKNIINDLRPEEFEEF
 EOLDPKPOVSGSRPVIKPEVDSFGCHNYVPIOTLCKRKELKKVNNNIPDVLKDLSTYKNIINDLRPEEFEEF
 220 230 240 250 260 270 280

230	300	310	320	330	340	350	360	370
DVHEKTLKLNSSN	IEEIDPAAGLTHLEEDLN	NNNSLNFGYGL	EDLYF	KLML	EDNRC	DYNI	HYTH	
235	300	310	320	330	340	350	360	370
DVHEKTLKLNSSN	IEEIDPAAGLTHLEEDLN	NNNSLNFGYGL	EDLYF	KLML	EDNRC	DYNI	HYTH	

YUMLKHNHNFNELEKTEPEEYKGVSGV	370	380	390	400	410	420	430
YSRYSEECRKDLPA							
PSFPDDIEDDEWEK							
RHNDHPAKK							
YUMLKHNHNFNELEKTEPEEYKGVSGV	370	380	390	400	410	420	430
INSYIEECPKDLPA							
PSFPDDIEDDEWEK							
RHNDHPAKK							

X
SVITIVG
IIIIIIII
SVITIVG
440

2. US-09-894-657-3 (1-440)
US-09-894-657-8 Sequence 8, Application US/09894657

Initial Score	=	229	Optimized Score	=	305	Significance	=	0.62
Residue Identity	=	98%	Matches	=	307	Mismatches	=	2
Gaps	=	1	Conservative Substitutions	=			=	3

X 10 20 30 40 50 60 70
M R V T I V L I C F C K A E L R K S P G S V R S K Y N H G R A G G R G S N P V K R Y A R P L P C D Y Y T Y L H E K Y L D C Q E R K L

